



SEQUENCE LISTING

<110> Yamaguchi, Shotaro

<120> NOVEL PROTEIN-DEAMIDATING ENZYME, MICROORGANISM PRODUCING THE SAME, GENE ENCODING THE SAME, PRODUCTION PROCESS THEREFOR, AND USE THEREOF

<130> A20-128923C

<150> JP Hei. 11-345044

<151> 1999-12-03

<160> 11

<170> PatentIn version 3.0

<210> 1

<211> 20

<212> PRT

<213> Cryseobacterium sp. No. 9670

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Leu Ala Ser Val Ile Pro Asp Val Ala Thr Leu Asn Ser Leu Phe Asn
1 5 10 15

Gln Ile Lys Asn
20

<210> 2

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<212> PRT

<213> Cryseobacterium sp. No. 9670

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Ser Pro Ser Asn Ser Tyr Leu Tyr Asp Asn Asn Leu Ile Asn Thr Asn
1 5 10 15

Cys Val Leu Thr
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<210> 3

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<212> DNA

<213> Artificial/Unknown

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<223> n = G, A, T or C

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gcnwsngtna thccngaygt

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arnacrcart tngtrtttdat

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cagtcttgcg gtacctctac ggcgctctca ccatgcatca cattcagata tcctgtagac	120
ggatgttatg caagagccca taagatgaga caaatcttaa tgaacaacgg ctatgactgt	180
gaaaaacaat ttgtatacgg aaacctaaag gcatcaacag gaacttgctg tgtggcgtgg	240
agctaccacg ttgcaatatt ggtaagctat aaaaatgott ccggagtaac ggaaaaaaga	300
attattgacg cttcactatt ttcaagcggg cctgtaacag atacagcatg gagaaacgct	360
tgcgttaaca cctcttgagg atctgcatcc gtttctctt atgctaatac tgcaggaaat	420
gtttattaca gaagtcctag taattcttac ctgtatgaca acaatctgat caataccaac	480
tgtgtactga ctaaattttc actgctttcc ggatgttctc cttcacctgc accggatgta	540
tccagctgtg gattt	555

<210> 6
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 <212> PRT
 <213> Cryseobacterium sp. No. 9670

<400> 6

Leu Ala Ser Val Ile Pro Asp Val Ala Thr Leu Asn Ser Leu Phe Asn	1	5	10	15
Gln Ile Lys Asn Gln Ser Cys Gly Thr Ser Thr Ala Ser Ser Pro Cys	20	25	30	
Ile Thr Phe Arg Tyr Pro Val Asp Gly Cys Tyr Ala Arg Ala His Lys	35	40	45	
Met Arg Gln Ile Leu Met Asn Asn Gly Tyr Asp Cys Glu Lys Gln Phe	50	55	60	
Val Tyr Gly Asn Leu Lys Ala Ser Thr Gly Thr Cys Cys Val Ala Trp	65	70	75	80
Ser Tyr His Val Ala Ile Leu Val Ser Tyr Lys Asn Ala Ser Gly Val	85	90	95	
Thr Glu Lys Arg Ile Ile Asp Pro Ser Leu Phe Ser Ser Gly Pro Val	100	105	110	
Thr Asp Thr Ala Trp Arg Asn Ala Cys Val Asn Thr Ser Cys Gly Ser	115	120	125	
Ala Ser Val Ser Ser Tyr Ala Asn Thr Ala Gly Asn Val Tyr Tyr Arg	130	135	140	
Ser Pro Ser Asn Ser Tyr Leu Tyr Asp Asn Asn Leu Ile Asn Thr Asn	145	150	155	160

Cys Val Leu Thr Lys Phe Ser Leu Leu Ser Gly Cys Ser Pro Ser Pro
165 170 175

Ala Pro Asp Val Ser Ser Cys Gly Phe
180 185

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<213> Cryseobacterium sp. No. 9670

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atg aaa aat ctt ttt tta tca atg atg gcc ttt gtg acc gtc tta 105
Met Lys Asn Leu Phe Leu Ser Met Met Ala Phe Val Thr Val Leu
-135 -130 -125

act ttt aat tcc tgt gcc gat tcc aac ggg aat cag gaa atc aac 150
Thr Phe Asn Ser Cys Ala Asp Ser Asn Gly Asn Gln Glu Ile Asn
-120 -115 -110

gga aag gaa aaa cta agt gta aat gat tct aag ctg aaa gat ttc gga 198
Gly Lys Glu Lys Leu Ser Val Asn Asp Ser Lys Leu Lys Asp Phe Gly
-105 -100 -95

aag act gta ccg gta ggg ata gac gaa gaa aac gga atg ata aag gtg 246
Lys Thr Val Pro Val Gly Ile Asp Glu Glu Asn Gly Met Ile Lys Val
-85 -80 -75

tca ttt atg tta act gcg caa ttc tat gaa att aag ccg acc aaa gaa 294
Ser Phe Met Leu Thr Ala Gln Phe Tyr Glu Ile Lys Pro Thr Lys Glu
-70 -65 -60

aat gag cag tat atc gga atg ctt aga cag gct gtt aag aat gaa tct 342
Asn Glu Gln Tyr Ile Gly Met Leu Arg Gln Ala Val Lys Asn Glu Ser
-55 -50 -45

cct gta cac att ttc tta aag cct aat agc aat gaa ata gga aaa gtg 390
Pro Val His Ile Phe Leu Lys Pro Asn Ser Asn Glu Ile Gly Lys Val
-40 -35 -30

gag tct gca agt ccg gaa gac gta aga tat ttt aaa acg atc ctg aca 438
Glu Ser Ala Ser Pro Glu Asp Val Arg Tyr Phe Lys Thr Ile Leu Thr
-25 -20 -15 -10

aaa gaa gta aaa ggg caa acc aat aaa ttg gcg agt gta att cct gat 486
Lys Glu Val Lys Gly Gln Thr Asn Lys Leu Ala Ser Val Ile Pro Asp

	-5	-1	1		5	
gta gct aca tta aat tct tta ttc aat caa ata aag aat cag tct tgc						534
Val Ala Thr Leu Asn Ser Leu Phe Asn Gln Ile Lys Asn Gln Ser Cys						
	10		15		20	
ggt acc tot acg gcg tcc tca cca tgc atc aca ttc aga tat cct gta						582
Gly Thr Ser Thr Ala Ser Ser Pro Cys Ile Thr Phe Arg Tyr Pro Val						
	25		30		35	
gac gga tgt tat gca aga gcc cat aag atg aga caa atc tta atg aac						630
Asp Gly Cys Tyr Ala Arg Ala His Lys Met Arg Gln Ile Leu Met Asn						
	40		45		50	55
aac ggc tat gac tgt gaa aaa caa ttt gta tac gga aac cta aag gca						678
Asn Gly Tyr Asp Cys Glu Lys Gln Phe Val Tyr Gly Asn Leu Lys Ala						
		60		65		70
tca aca gga act tgc tgt gtg gcg tgg agc tac cac gtt gca ata ttg						726
Ser Thr Gly Thr Cys Cys Val Ala Trp Ser Tyr His Val Ala Ile Leu						
		75		80		85
gta agc tat aaa aat gct tcc gga gta acg gaa aaa aga att att gat						774
Val Ser Tyr Lys Asn Ala Ser Gly Val Thr Glu Lys Arg Ile Ile Asp						
	90		95		100	
cct tca cta ttt tca agc ggt cct gta aca gat aca gca tgg aga aac						822
Pro Ser Leu Phe Ser Ser Gly Pro Val Thr Asp Thr Ala Trp Arg Asn						
	105		110		115	
gct tgc gtt aac acc tct tgc gga tct gca tcc gtt tcc tct tat gct						870
Ala Cys Val Asn Thr Ser Cys Gly Ser Ala Ser Val Ser Ser Tyr Ala						
	120		125		130	135
aat act gca gga aat gtt tat tac aga agt cct agt aat tct tac ctg						918
Asn Thr Ala Gly Asn Val Tyr Tyr Arg Ser Pro Ser Asn Ser Tyr Leu						
		140		145		150
tat gac aac aat ctg atc aat acc aac tgt gta ctg act aaa ttt tca						966
Tyr Asp Asn Asn Leu Ile Asn Thr Asn Cys Val Leu Thr Lys Phe Ser						
		155		160		165
ctg ctt tcc gga tgt tct cct tca cct gca ccg gat gta tcc agc tgt						1014
Leu Leu Ser Gly Cys Ser Pro Ser Pro Ala Pro Asp Val Ser Ser Cys						
	170		175		180	
gga ttt taattaattg ataattttac agcacctgct catttacaga atcagcaggt						1070
Gly Phe						
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gctgttatat						1080

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Met Lys Asn Leu Phe Leu Ser Met Met Ala Phe Val Thr Val Leu
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Thr Phe Asn Ser Cys Ala Asp Ser Asn Gly Asn Gln Glu Ile Asn
-120 -115 -110

Gly Lys Glu Lys Leu Ser Val Asn Asp Ser Lys Leu Lys Asp Phe Gly
-105 -100 -95 -90

Lys Thr Val Pro Val Gly Ile Asp Glu Glu Asn Gly Met Ile Lys Val
-85 -80 -75

Ser Phe Met Leu Thr Ala Gln Phe Tyr Glu Ile Lys Pro Thr Lys Glu
-70 -65 -60

Asn Glu Gln Tyr Ile Gly Met Leu Arg Gln Ala Val Lys Asn Glu Ser
-55 -50 -45

Pro Val His Ile Phe Leu Lys Pro Asn Ser Asn Glu Ile Gly Lys Val
-40 -35 -30

Glu Ser Ala Ser Pro Glu Asp Val Arg Tyr Phe Lys Thr Ile Leu Thr
-25 -20 -15 -10

Lys Glu Val Lys Gly Gln Thr Asn Lys Leu Ala Ser Val Ile Pro Asp
-5 -1 1 5

Val Ala Thr Leu Asn Ser Leu Phe Asn Gln Ile Lys Asn Gln Ser Cys
10 15 20

Gly Thr Ser Thr Ala Ser Ser Pro Cys Ile Thr Phe Arg Tyr Pro Val
25 30 35

Asp Gly Cys Tyr Ala Arg Ala His Lys Met Arg Gln Ile Leu Met Asn
40 45 50 55

Asn Gly Tyr Asp Cys Glu Lys Gln Phe Val Tyr Gly Asn Leu Lys Ala
60 65 70

Ser Thr Gly Thr Cys Cys Val Ala Trp Ser Tyr His Val Ala Ile Leu
75 80 85

Val Ser Tyr Lys Asn Ala Ser Gly Val Thr Glu Lys Arg Ile Ile Asp
90 95 100

Pro Ser Leu Phe Ser Ser Gly Pro Val Thr Asp Thr Ala Trp Arg Asn
105 110 115

Ala Cys Val Asn Thr Ser Cys Gly Ser Ala Ser Val Ser Ser Tyr Ala
120 125 130 135

Asn Thr Ala Gly Asn Val Tyr Tyr Arg Ser Pro Ser Asn Ser Tyr Leu
140 145 150

Tyr Asp Asn Asn Leu Ile Asn Thr Asn Cys Val Leu Thr Lys Phe Ser
155 160 165

Leu Leu Ser Gly Cys Ser Pro Ser Pro Ala Pro Asp Val Ser Ser Cys
170 175 180

Gly Phe
185

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cagaattcat gaaaaatcctt tttttatcaa tggcc

35

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29